Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 05:34:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548986.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1548986 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548986.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 05:34:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548986.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,775,632
Mapped reads	4,349,985 / 44.5%
Unmapped reads	5,425,647 / 55.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	101,616 / 1.04%
Duplication rate	1.41%
Clipped reads	402,265 / 4.11%

2.2. ACGT Content

Number/percentage of A's	50,554,915 / 29.43%
Number/percentage of C's	34,981,850 / 20.36%
Number/percentage of T's	50,948,582 / 29.66%
Number/percentage of G's	35,306,109 / 20.55%
Number/percentage of N's	8,761 / 0.01%
GC Percentage	40.91%

2.3. Coverage

Mean	0.0555
Standard Deviation	0.4284

2.4. Mapping Quality

Mean Mapping Quality	42.28

2.5. Mismatches and indels

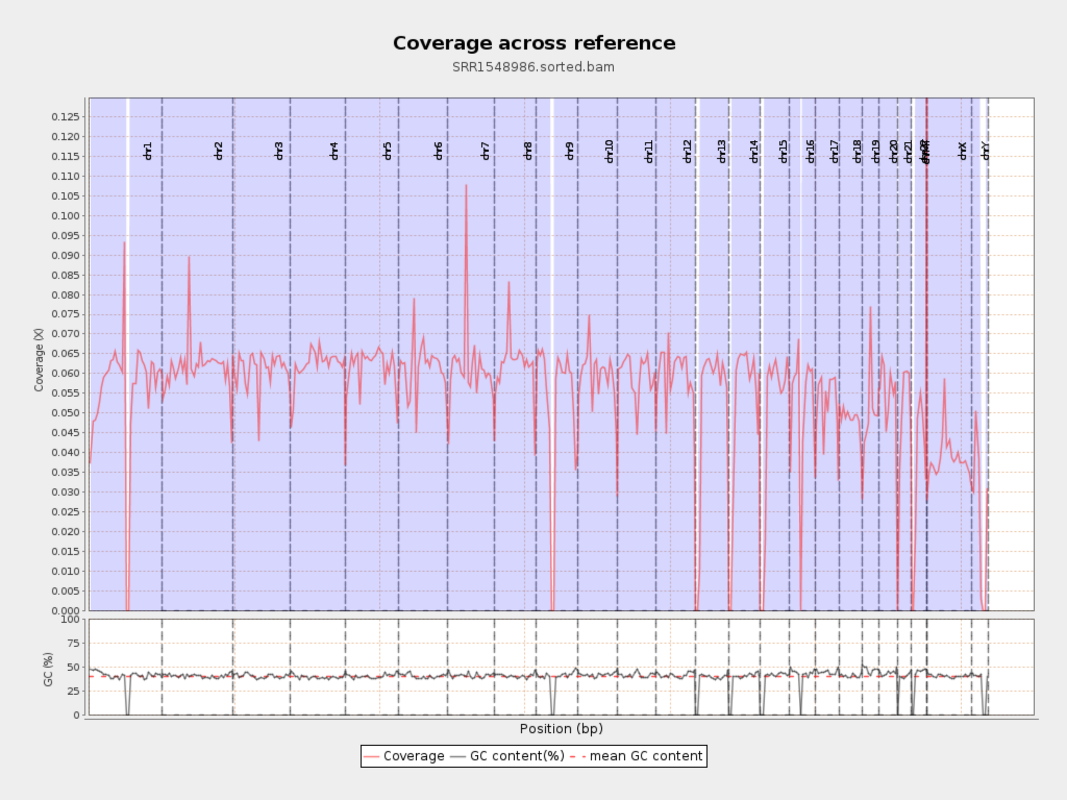
General error rate	0.32%
Mismatches	536,549
Insertions	6,667
Mapped reads with at least one insertion	0.15%
Deletions	16,560
Mapped reads with at least one deletion	0.38%
Homopolymer indels	43.05%

2.6. Chromosome stats

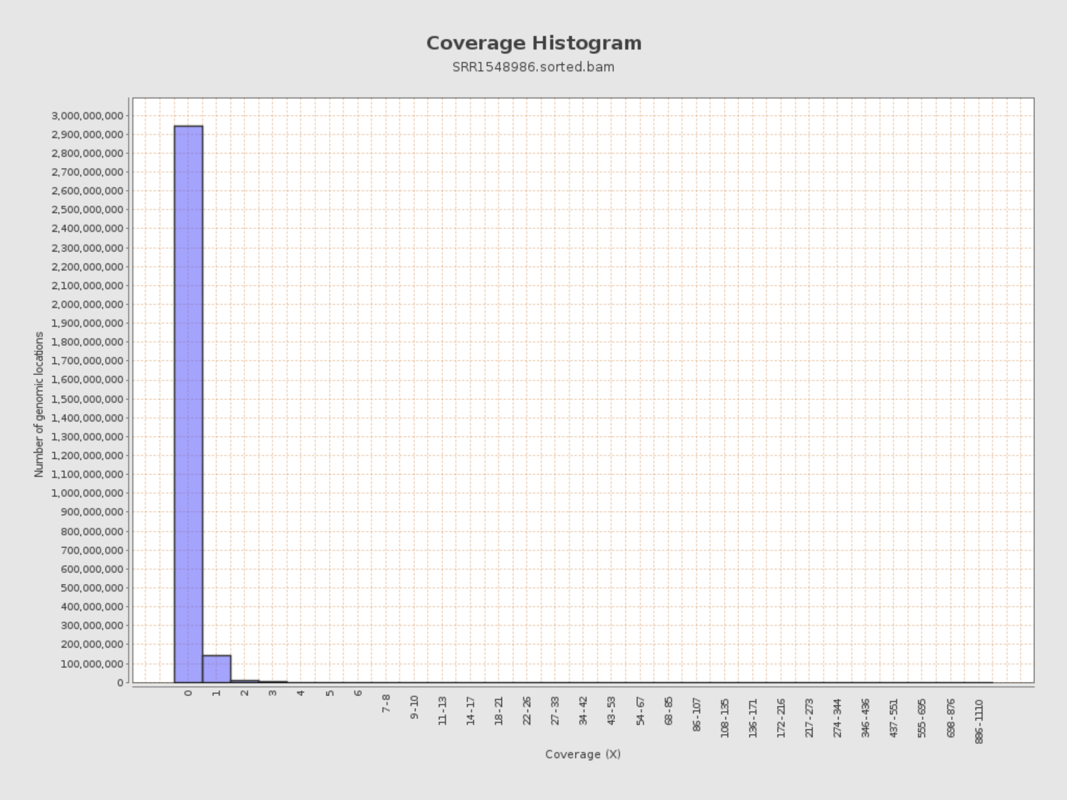
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13857489	0.0556	0.8345
chr2	243199373	15018022	0.0618	0.3852
chr3	198022430	12118672	0.0612	0.2675
chr4	191154276	11894500	0.0622	0.2739
chr5	180915260	11200792	0.0619	0.2752
chr6	171115067	10530185	0.0615	0.3369
chr7	159138663	9924937	0.0624	0.6977
chr8	146364022	9134275	0.0624	0.5363

chr9	141213431	7373974	0.0522	0.3564
chr10	135534747	8144715	0.0601	0.3424
chr11	135006516	8000593	0.0593	0.3577
chr12	133851895	8008346	0.0598	0.2753
chr13	115169878	5831318	0.0506	0.2413
chr14	107349540	5430937	0.0506	0.2983
chr15	102531392	4924271	0.048	0.238
chr16	90354753	4616436	0.0511	0.2666
chr17	81195210	4238917	0.0522	0.2787
chr18	78077248	3802256	0.0487	0.5946
chr19	59128983	2996786	0.0507	0.7
chr20	63025520	3467824	0.055	0.2626
chr21	48129895	2263672	0.047	0.2612
chr22	51304566	1708346	0.0333	0.2484
chrMT	16571	2818	0.1701	0.4411
chrX	155270560	5988976	0.0386	0.2661
chrY	59373566	1341877	0.0226	0.2097

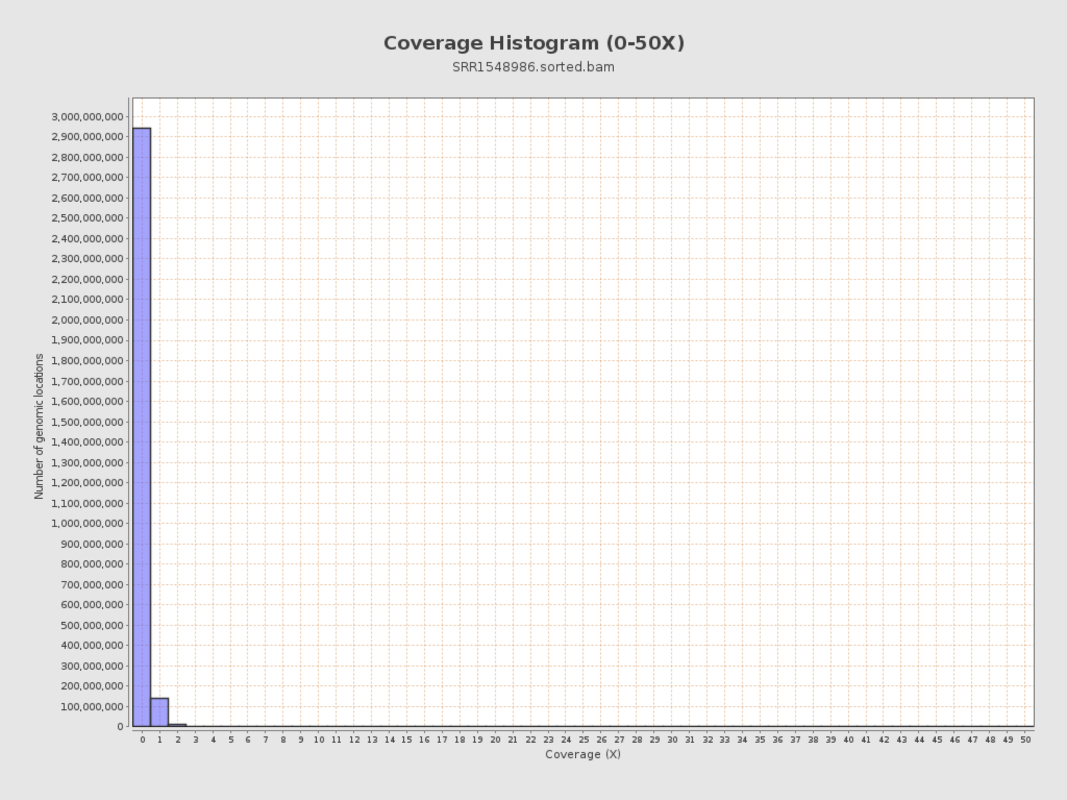
3. Results : Coverage across reference



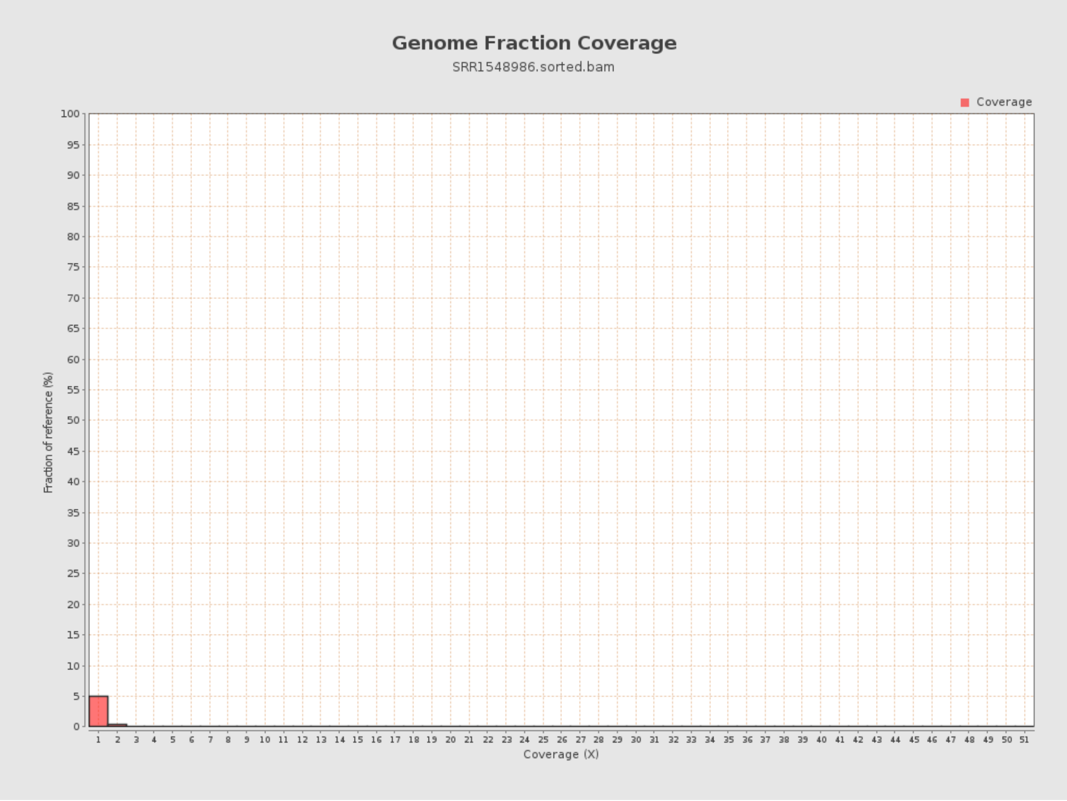
4. Results : Coverage Histogram



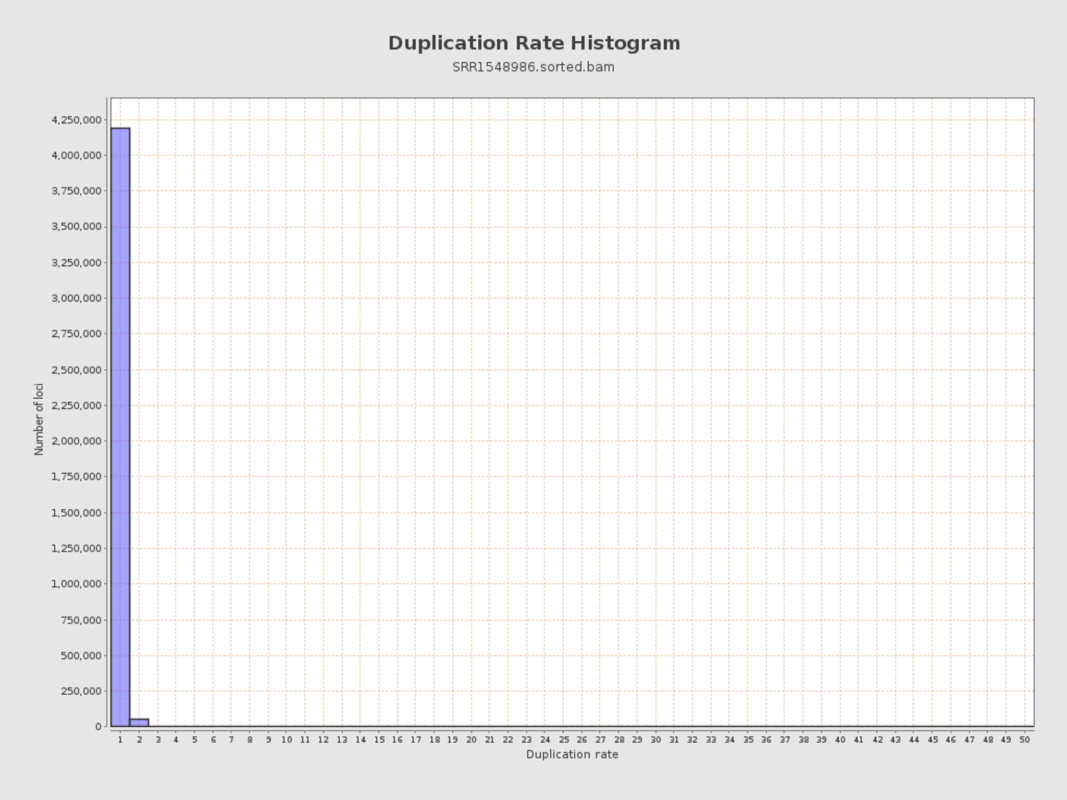
5. Results : Coverage Histogram (0-50X)



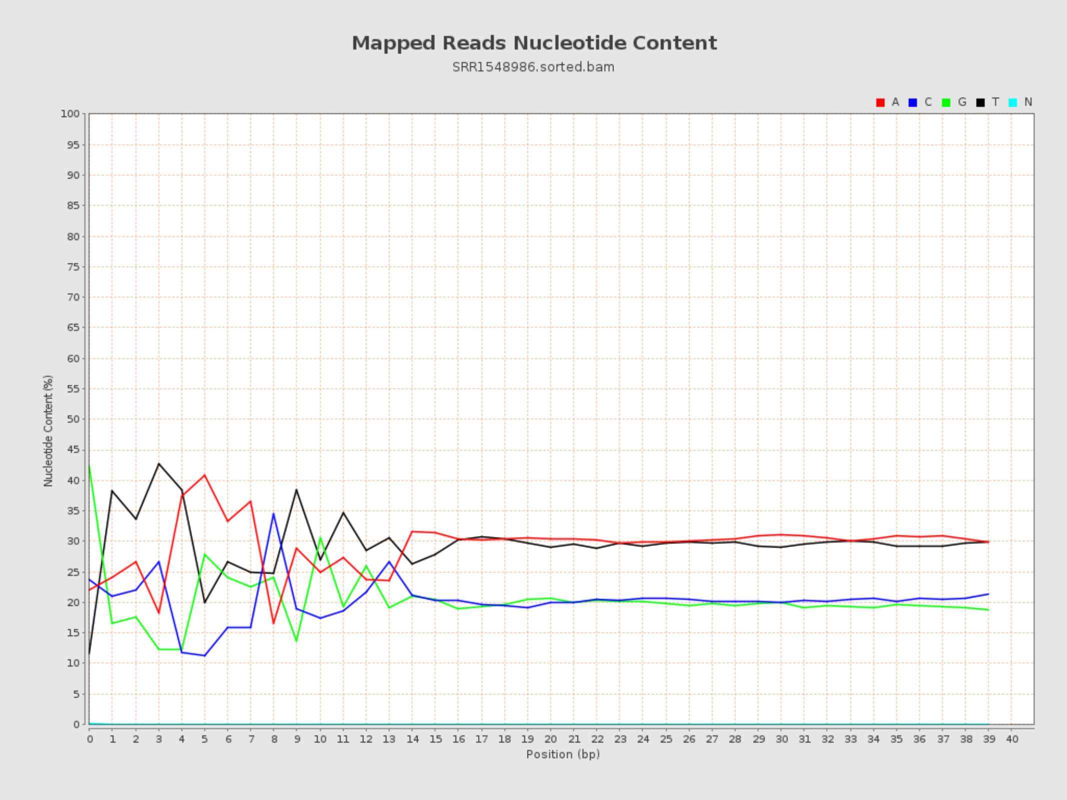
6. Results : Genome Fraction Coverage



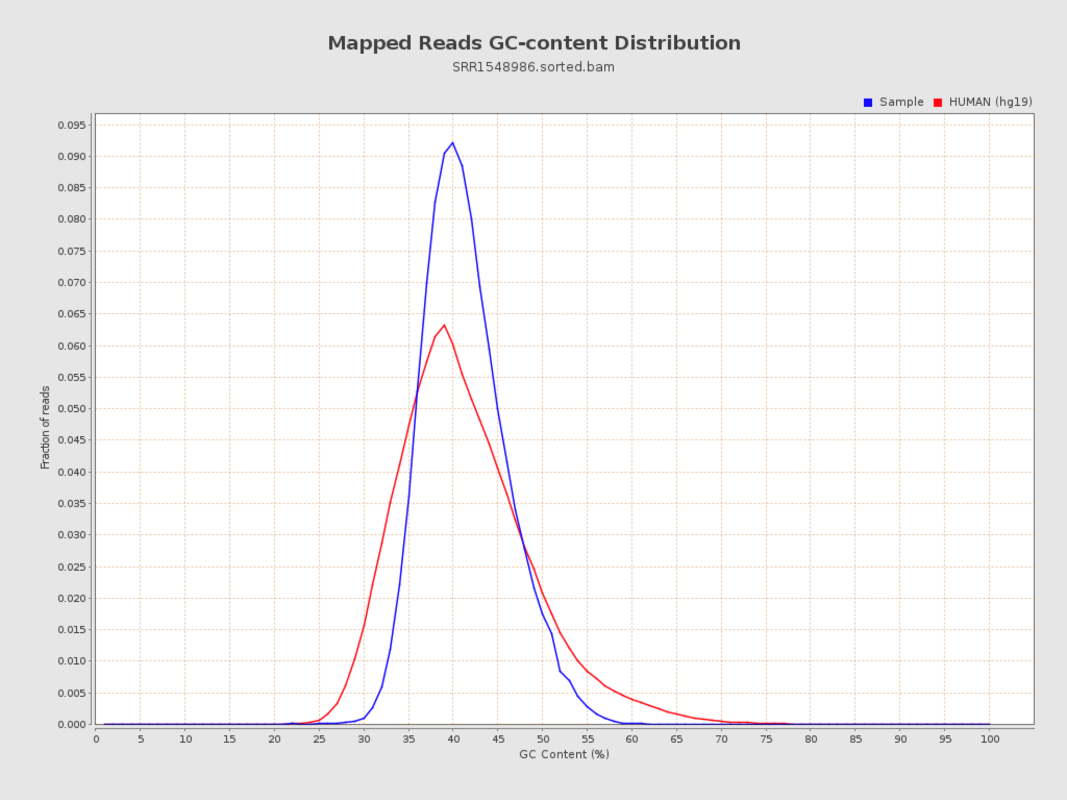
7. Results : Duplication Rate Histogram



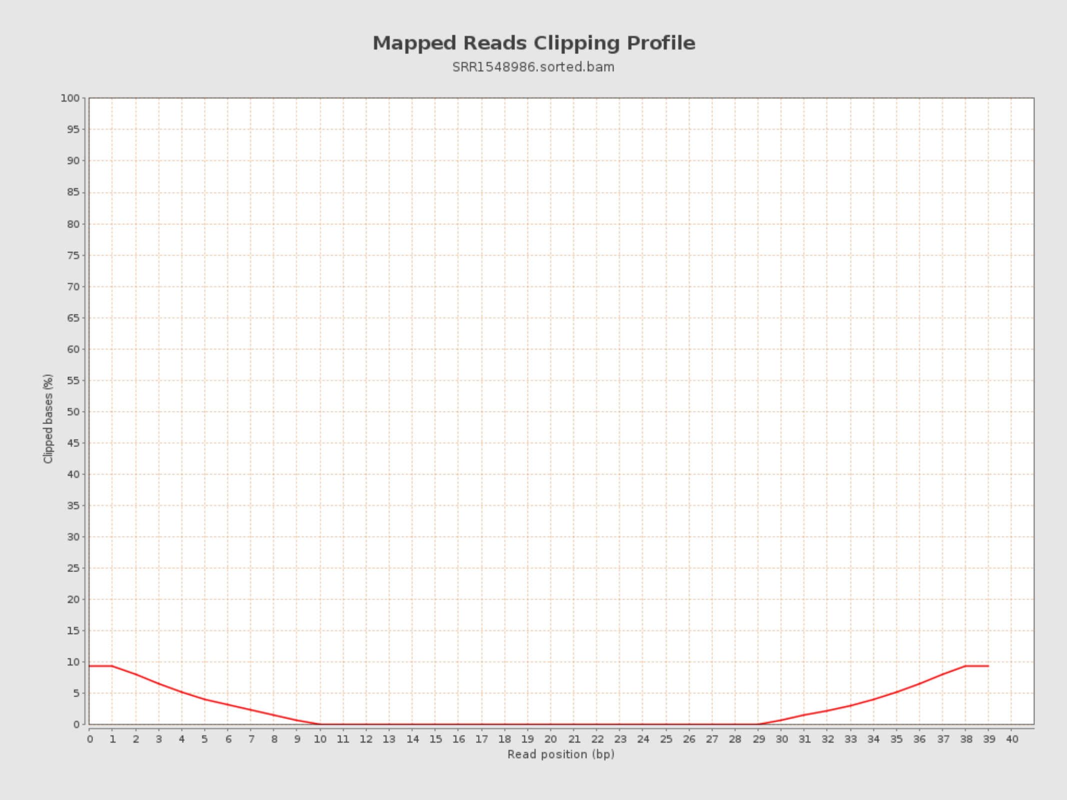
8. Results : Mapped Reads Nucleotide Content



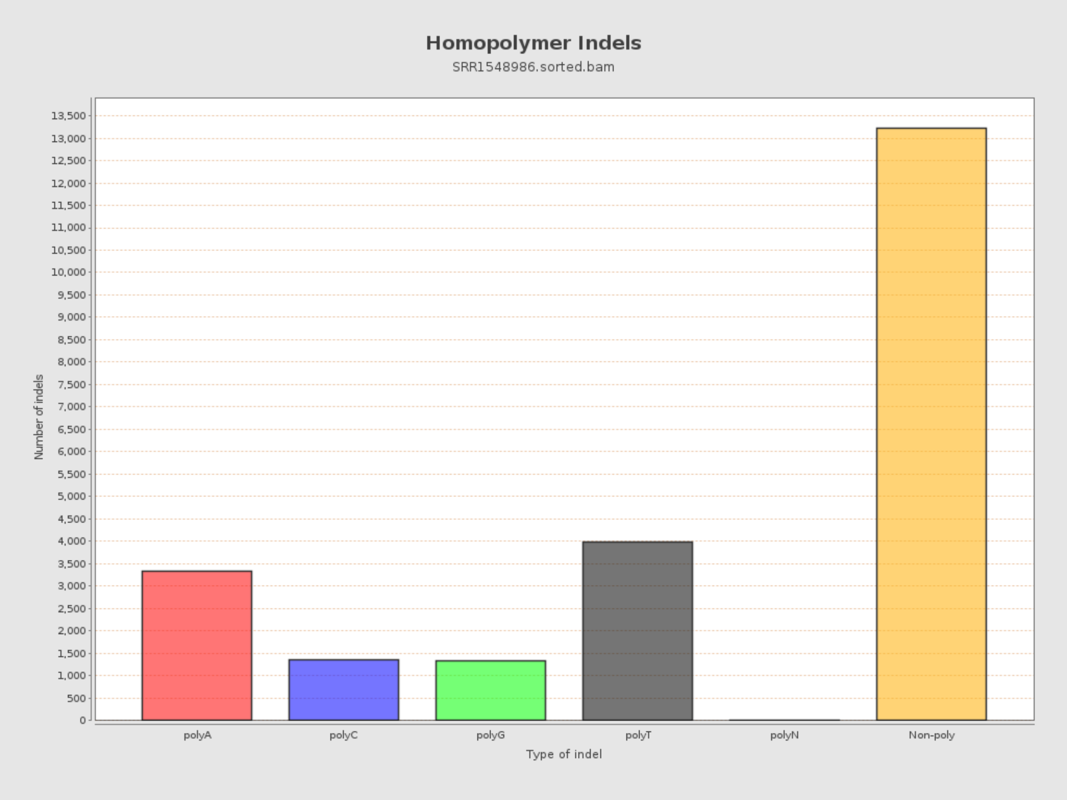
9. Results : Mapped Reads GC-content Distribution



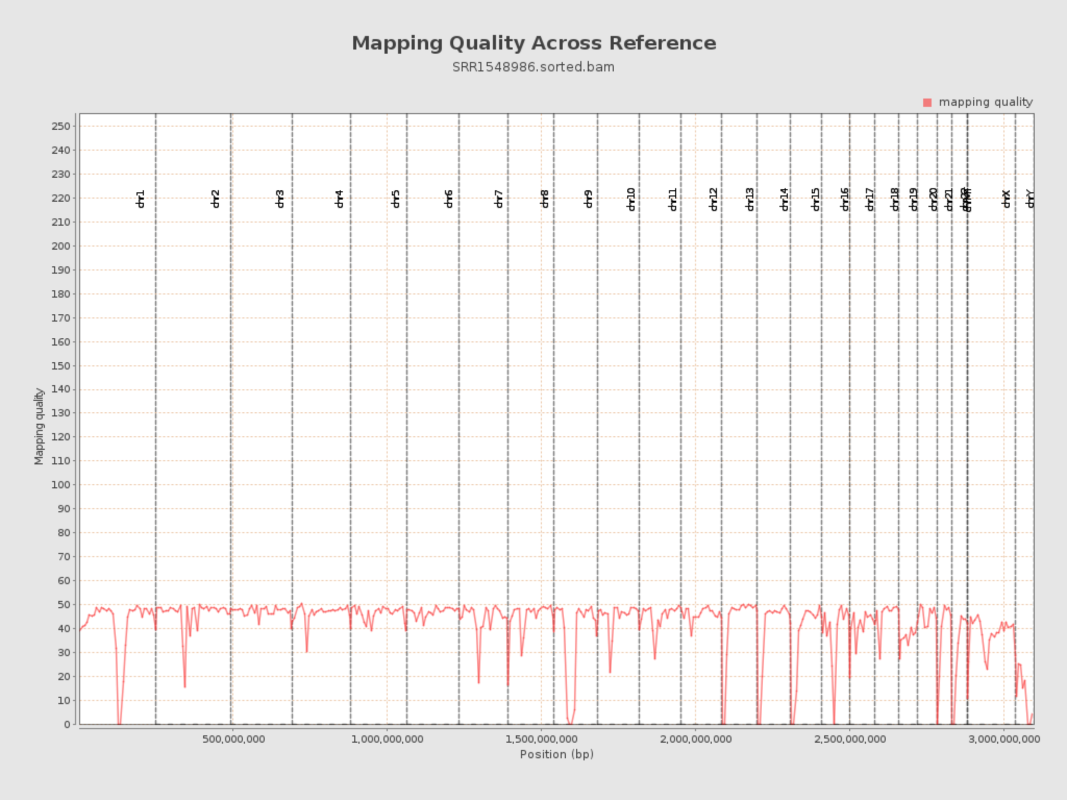
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram